

# Supplementary Information

**Figure S1.** Open reading frame and amino acid sequence of the *GhLRP* gene. (A) Open reading frame sequence of the *GhLRP* gene; (B) GhLRP protein sequence; (C) Amino acid composition of the GhLRP protein.

(A)

1	ATGATCGGTA	GCCACACCGT	CTCGTCAACG	ACTCGACATT	TATTCCAGAC	ACAAACAACC
61	TCATCAGAGC	TGCCACAATT	GGCTTCAAAA	TACAAAAAGC	ACGAAGAGTC	TGAATACAAA
121	CAGCCAAAAT	ATCACGAAGA	GCACCCAAAA	CATGAGAAGC	CTGAAATGCA	CAAGGAGGAA
181	AGACAAAAAC	CCTACAAACA	ACATGAAGAG	TACCACGAGT	CACACGAATC	GAAGAAGCAC
241	GAAGAGTACA	ATAAAGACAA	ACCCGATTTC	CCCAAATGGG	AAAAGCCTAA	AGAGCACGAG
301	AAACACGAAG	TCGAATATCC	GAAAATACCC	GAGTACAAGG	ACAAACAAGA	TGAGGATAAG
361	GAACATAAAA	ATGAAGAGTT	CCACGAATCA	CGCGAATCAA	AGGAGCACAA	AGAGTATGAG
421	AAAGAAAAAC	CCGAGTTCCC	CAAACAGCAA	AAGCCTAAAG	AGCACGAGAA	ACACCAAGTC
481	GAATATCCGG	AAATAACCCA	GTACAAGGAA	GAGCAAGATA	AGAGTAAGGA	ACATAAAGAT
541	GAAGAGTGCC	ACGAGTCACA	CGAATCGAAA	GAGCACGAAG	AGTACTAG	

(B)

1	MIGSHTVSST	TRHLFQTQTT
21	SSELPQLASK	YKKHEESEYK
41	QPKYHEEHPK	HEKPEMHKEE
61	RQKPYKQHEE	YHESHEKKH
81	EEYNKDKPDF	PKWEKPKHEE
101	KHEVEYPKIP	EYKDKQDEDK
121	EHKNEEFHES	RESKEHKEYE
141	KEKPEFPKQQ	KPKEHEKHQV
161	EYPEITQYKE	EQDKSKEHKD
181	EECHESHESK	EHEEY*

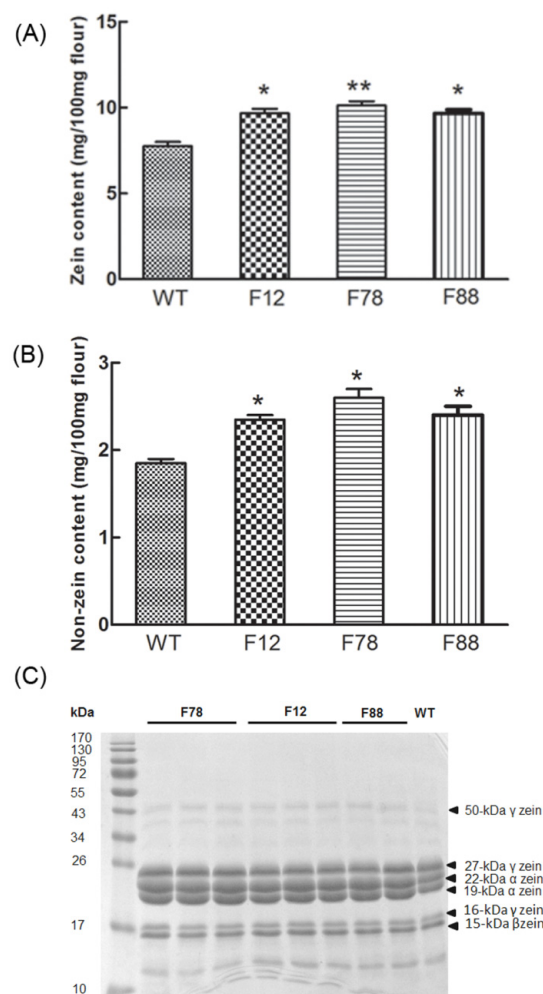
(C)

Amino acid	Num	%w/w
A Ala	1	0.32
C Cys	1	0.44
D Asp	7	3.36
E Glu	47	24.93
F Phe	4	2.38
G Gly	1	0.27
H His	22	12.30
I Ile	3	1.42
K Lys	36	18.97
L Leu	3	1.42
M MET	2	1.08
N Asn	2	0.95
P Pro	14	5.81
Q Gln	12	6.32
R Arg	3	1.88
S Ser	14	5.30
T Thr	7	3.01
V Val	3	1.27
W Trp	1	0.74
Y Tyr	12	7.84

**Figure S2.** Selection of maize resistant callus and plant regeneration. (A) Maize callus on selection medium containing 15 mg/L hygromycin; (B) Differentiation of resistant callus; (C) Regenerated plants in the rooting medium; (D) Regenerated plants in a flowerpot; (E) Regenerated plants in the field; (F) T<sub>0</sub> transgenic maize seeds.



**Figure S3.** Zein and non-zein accumulation pattern in T<sub>4</sub> kernels of three transgenic lines. (A) Zein content; (B) Non-zein content. All the calculations were performed with technical triplicates and biological triplicates, and 20 mature kernels were used per assay. Student's *t*-test is used to evaluate the difference between the transgenic maize and WT (\* *p* < 0.05; \*\* *p* < 0.01); (C) Zein proteins of WT, F12, F78, and F88 lines were analyzed by SDS-PAGE. For SDS-PAGE, 5 µL samples were loaded to 15% polyacrylamide gel. The size for each protein marker and sample band was indicated by the numbers in the “kDa” columns.



**Table S1.** Agronomic traits of T<sub>3</sub> kernels in three transgenic lines.

Line	PH (cm)	EH (cm)	EL (cm)	BTL (cm)	ED (cm)	ER	KW (g)
F12	200.7 ± 3.2	98.7 ± 5.4	11.8 ± 1.8	1.0 ± 0.7	37.7 ± 0.8	14	24.4 ± 0.9
F78	198.5 ± 7.5	89.3 ± 5.8	13.2 ± 1.6	0.4 ± 0.3	42.7 ± 1.2	16	25.2 ± 1.2
F88	210.3 ± 4.2	92.3 ± 4.2	12.0 ± 1.3	1.9 ± 1.4	39.2 ± 2.8	14	27.3 ± 3.4
WT <sup>a</sup>	202.5 ± 5.8	89.3 ± 3.8	11.3 ± 2.3	0.7 ± 0.6	39.8 ± 0.3	16	26.8 ± 4.0

<sup>a</sup> The segregating populations of hybrid 08 × 178 in T<sub>3</sub> were used as a control (WT). PH, plant height; EH, ear height; EL, ear length; BTL, bald tip length; ED, ear diameter; ER, number of ear rows; KW, 100-kernel weight. Values are average measurements for each line in T<sub>2</sub> progenies ± standard deviation. Differences in agronomic traits between transgenic lines and WT were analyzed using a Student's *t*-test.